



SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: de la Torre, Juan C.

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING  
OF HUMAN BORNA DISEASE VIRUS

10

(iii) NUMBER OF SEQUENCES: 65

(iv) CORRESPONDENCE ADDRESS:

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- (A) ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
- (B) STREET: 10550 North Torrey Pines Road, TPC-8
- (C) CITY: La Jolla
- (D) STATE: California
- (E) COUNTRY: United States
- (F) ZIP: 92037

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(v) COMPUTER READABLE FORM:

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- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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- (A) APPLICATION NUMBER: US
- (B) FILING DATE: 7-JAN-1997
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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- (A) NAME: Fitting, Thomas
- (B) REGISTRATION NUMBER: 34,163
- (C) REFERENCE/DOCKET NUMBER: TSRI 465.0

(ix) TELECOMMUNICATION INFORMATION:

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- (A) TELEPHONE: (619) 784-2937
- (B) TELEFAX: (619) 784-9399

(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	GTTCGCTTAA CAACAAACCA MTCATYATYC TTCTAACAAA ATGAACACAC GCAATGCCAC	60
10	CCAAGAGACG CCTGGTTGAT GACGCCGATG CCATGGAGGA YCAAGATYTA TATGAACCCC	120
	CAGCGAGCCT CCCYAAGCTC CCYGGRAAAT TCCTACAATA CACCGTTGGG GGGTCTGACC	180
15	CGCATCCGGG TATAGGGCAT GAGAARGAYA TCAGGCAGAA CGCAGTGGCA TTGTTAGACC	240
	AGTCACGGCG CGATATGTTT CAYACAGTAA CGCCYAGCCT TGTGTTTCTA TGTTTGCTAA	300
	TCCCAGGACT GCACGCTGCG TTTGTTTACG GAGGGGTGCC TCGTGAATCY TACCTGTCTGA	360
20	CGCCTGTYAC GCGTGGRGAA CAGACTGTYG TTAAGACTGC RAAGTTTTAC GGGGAAAAGA	420
	CRACRCAGCG TGATCTCACC GAGCTGGAGA TCTCCTCTAT MTTCAGCCAT TGTGCTCAT	480
25	TACTAATWGG GGTGTGATA GGATCGTCRT CTAAGATYAA AGCAGGAGCC GAGCAGATCA	540
	AGAAAAGGTT TAAAACTATG ATGGCAGCCT TAAACCGGCC ATCCCATGGT GAGACTGCTA	600
	CACTACTYCA GATGTTTAAAT CCACATGAGG CTATAGATTG GATTAACGGC CARCCCTGGG	660
30	TAGGCTCCTT TGTGTTGTCT CTACTAACTA CAGACTTTGA GTCCCCAGGT AAAGAATTYA	720
	TGGAYCAGAT TAARCTTGTC GCAAGTTATG CRCAGATGAC TACGTACACT ACTATAAAGG	780
35	AGTACCTCGC AGAATGYATG GATGCTACCC TTACAATCCC YGTAGTTGCA TATGAGATYC	840
	GTGACTTTTT AGAAGTTTCA GCAAAGCTTA ARGAGGAWCA TGCTGACCTG TTYCCGTTYC	900
	TGGGGGCGYAT TMGRCAACCC GACGCTATCA AGCTKGGGCC ACGRAGCTTT CCCAATCTGG	960
40	CYTCYGCAGC GTTTTACTGG AGTAAGAAGG ARAAYCCAC AATGGCRGGC TACCGGGCCT	1020
	CCACCATCCA GCGGGGCGCR AGTGTCAGG ARACCCAGCT TGCCCGGTAT AGGCGCCGCG	1080
45	AGATATCTCG YGGRGARGAC GGGGCAGAGC TCTCAGGTGA GATCTCTGCC ATAATGARRA	1140
	TGATAGGTGT GACTGGTCTA AACTARAAAA CAATGAACAA ACCAATAAAA AACCAAATGC	1200
	GGCAAACCCY CCGCGACCTG YGATGAGYTC CGACCTCCGG CTGACATTGC TTGAAYTAGT	1260
50	CAGGAGGCTC AATGGCAACG SGACCATCGA GTCTGGTCTGA CTCCCTGGAG GACGAAGAAG	1320

	ATCCCCAGAC	ACTACGACGG	GAACGAYCGG	GGTCACCAAG	ACCACGGAAG	RTCCCAAGGA	1380
	ATGCATTGAC	CCAACCRGTA	GACCAGCTCC	TGAAGGACCT	CAGGAAGAAC	CCCTCCATGA	1440
5	TCTCAGACCC	AGACCAGCGA	ACCGGAAGGG	AGCAGCTRTC	GAATGATGAG	CTWATCAAGA	1500
	AGYTAGTGAC	GGAGCTGGCC	GAGAATAGCA	TGATCGAGGC	TGAGGAGGTG	CGGGGCACTC	1560
	TTGGRGACAT	CTCGGCTCGY	ATCGAGGCAG	GGTTTGAGTC	CCTGTCCGCC	CTCCAAGTGG	1620
10	AAACCATCCA	GACAGCTCAG	CGGTGCGAYC	ACTCCGAYAG	CATCAGRATC	CTYGGCGAGA	1680
	ACATCAAGAT	ACTRGATCGC	TCCATGAAGA	CAATGATGGA	GACAATGAAG	CTCATGATGG	1740
15	AGAAGGTGGA	YCTCCTCTAC	GCATCAACCG	CCGTTGGGAC	CTCTGCACCC	ATGTTGCCCT	1800
	CCCATCCTGC	ACCTCCGCGC	ATTTATCCCC	AGCTCCCAAG	TGCCCCGACA	RCGGATGART	1860
	GGGACATCAT	ACCATAAAAA	AATCGAATCA	CCATGAATTC	AAARCATTCC	TATGTGGAGC	1920
20	TCAAGGRCAA	GGTAATCGTC	CCTGGATGGC	CCACACTGAT	GCTTGAGATA	GACTTTGTAG	1980
	GRGGGACTTC	ACGGAACCAG	TTCCTTAACA	TCCCATTCTT	TTCAGTGAAA	GAGCCTCTGC	2040
25	AGCTTCCACG	CGAGAAGAAG	TTGACCGACT	ACTTYACYAT	TGACGTAGAR	CCAGCAGGTC	2100
	ATTCCCTGGT	CAAYATATAC	TTCCAGATTG	ACGACTTCTT	GCTCCTAACA	CTCAACTCAC	2160
	TRTCYGTRTA	CAAGGACCCG	ATTAGRAAAT	ACATGTTCTT	ACGCCTCAAC	AAGGAMCAGA	2220
30	GCAAGCACGC	AATYAATGCA	GCYTTCAATG	TCTTYTCTTA	TCGGCTTCGG	AACATTGGTG	2280
	TTGGYCCTCT	CGGCCCCRGAC	ATTCGATCTT	CAGGGCCTTA	GYTGCAATAC	TGACTCCACT	2340
35	CCTGGAYTRA	TYGAYCTGGA	GATAAGGCGA	CTTTGCCACA	CCCCAACGGA	AAATGTCATT	2400
	TCATGCGAGG	TTAGTTATCT	YAACCACACG	ACTATTAGCC	TCCCGGCAGT	CCACACRTCA	2460
	TGCCTCAAGT	ACCACTGCAA	AACCTATTGG	GGATTCTTTG	GTAGCTACAG	CGCTGACCGA	2520
40	ATCATMAATC	GGTACACTGG	TACTGTAAAG	GGTTGTYTAA	ACAACTCAGC	RCCAGAGGAY	2580
	CCCTTCGAGT	GCAACTGGTT	CTACTGCTGC	TCGGCGATTA	CAACAGAGAT	CTGCCGATGC	2640
45	TCTATTACAA	ATGTCACGGT	GGCTGTRCAR	ACATTCCCAC	CGTTCATGTA	CTGCAGTTTY	2700
	GCRGACTGYA	GTACYGTGAG	YCARCAGGAG	CTAGAGAGTG	GMAAGGCAAT	GCTGAGCGAT	2760
	GGCAGTACMT	TAACTTATAC	CCCGTATATC	YTACARTCAG	AAGTCGTGAA	CAAAACCCTY	2820
50	AATGGGACYA	TACTCTGCAA	CTCATCCTCY	AAGATAGTTT	CCTTCGATGA	ATTAGGCGT	2880

	TCATACTCCC	TARCGAATGG	TAGTTACCAG	AGCTCATCAA	TCAATGTGAC	GTGTGYAAAC	2940
	TACACGTCGT	CCTGCCGGYC	CARGTTGARA	AGGCGGCGTA	GGGAYACYCA	RCAGATTGAG	3000
5	TAYCTAGTTC	ACAAGCTTAG	GCCYACACTG	AAAGATGCRT	GGGAGGACTG	TGAGATCCTC	3060
	CAGTCTCTGC	TCCTAGGGRT	GTTTGGTACT	GGGATYGCAA	GTGCTTCKCA	ATTYTTGAGG	3120
	RGCTGGCTCA	ACCACCCTGA	YATCATCGGG	TATATAGTTA	ATGGAGTTGG	GGTWGTCTGG	3180
10	CAATGCCATC	GTGTTAATGT	CACGTTCATG	GCGTGGAATG	AGTCCACMTA	TTACCCTCCA	3240
	GTAGATTACA	ATGGRCGGAA	GTACTTYCTG	AATGATGAGG	GRAGGYTACA	AACAAACACC	3300
15	CCCGAGGCAA	GGCCAGGGCT	TAAGCGGGTC	ATGTGGTTCG	GCAGGTACTT	CCTAGGGACA	3360
	GTAGGGTCTG	GGGTGAAACC	GAGGAGGATT	CGGTACAATA	AGACCTCACA	TGAYTACCAY	3420
	CTRGAGGAGT	TTGAGGCAAG	TCTCAACATG	ACCCCYCAGA	CCAGTATCGC	CTCGGGTCAT	3480
20	GAGACAGACC	CCATAAATCA	TGCCTACGGA	ACGCAGGCTG	AYCTCCTTCC	ATACACCAGG	3540
	TCTAGTAATA	TAAGRTCTAC	RGATACAGGC	TCAGGCTGGG	TGCACATCGG	CCTACCCTCA	3600
25	TTTGCTTTCC	TCAATCCYCT	CGGGTGGCTY	AGGGACCTAC	TTGCRITGGG	RGCCTGGTTG	3660
	GGTGGGGTTC	TATACTTAAT	AAGTCTTTGT	GTTTCCTTAC	CAGCCTCCTT	CGCGAGGAGG	3720
	AGACGCCTCG	GCCGGTGGCA	GGAATAAACC	GTACCGACCA	RWCTCTTAAA	AACCCTCTYC	3780
30	TCGGRACAGA	GGTCTCTTTC	TGCCTTAART	CGAGYTCACT	CCCCCATCAY	GTACGAGCAY	3840
	TRGGCCAGAT	TAAAGCAARG	AACCTGGCAT	CCTGTGACTA	TTACTTGCTA	TTCCGCCAAG	3900
35	TTGTATTGCC	CCCTGAAGTA	TATCCCATTG	GTGTYTAAT	AAGAGCTGGG	GAGGCYATAC	3960
	TAACAGTTAT	AGTATCAGCT	TGGAAGCTGG	ATCAYATGAC	RAAGACCCTA	TACTCCTCTG	4020
	TGAGATATGC	ACTCACCAAT	CCCCGGGTCC	GRGCCCCAAT	TGAGCTYCAC	ATTGCCTACC	4080
40	AGCGCATAGT	GGGTCAGGTC	TCGTAYAGCC	GGGARGCAGA	YATAGGGCCA	AAAAGGCTTG	4140
	GGAATATGTC	ATTGCAATTC	ATCCAATCYC	TCGTTATTGC	CACCATAGAC	ACRACRAGCT	4200
45	GCCTAATGAC	CTACAACCAC	TTTCTTGCTG	CAGCAGACAC	AGCCAAGAGC	AGATGCCAYC	4260
	TCCTAATCGC	CTCAGTGGTC	CARGGRGCCC	TTTGGGARCA	AGGGTCATTT	CTTGATCATA	4320
	TAATCAACAT	GATCGACAYA	ATTGACTCAA	TCAACCTCCC	CCATGATGAT	TACTTCACAA	4380
50	TTATTAAGTC	TATCTYTCCC	TACTCCCAAG	GGCTTGTTAT	GGGGAGGCAY	AATGTRTCAG	4440

	TCTCCTCTGA	TTTYGCGTCC	GTATTTTRCYA	TTCCTGAATY	ATGCCCRCAA	CTAGACAGCT	4500
	TACTAAAAAA	ACTGCTYCAA	CTTGACCCYG	TTCTCCTCCT	CATGGTCTCT	TCGGTGCAGA	4560
5	AGTCATGGTA	CTTCCCTGAG	ATCCGAATGG	TYGACGGGTC	ACGGGAGCAG	CTCCACAAGA	4620
	TGCGTGTCTGA	GCTGGARACG	CCCCAAGCCC	TGCTGTCRTA	CGGCCATACC	CTCCTGTCAA	4680
	TATTTTCGRGC	AGAGTTTATC	AAAGGCTATG	TCTCAAAGAA	TGCGAAGTGG	CGGCCYGTAC	4740
10	ACCTGCTCCC	AGGCTGTGAC	AAATCCATAA	ARAATGCGAG	AGAGCTGGGC	CGCTGGAGCC	4800
	CGGYRTTTGA	CCGACGATGG	CAGCTCTTCG	MGAAGGTTGT	CATTCTAAGA	ATTGCTGACC	4860
15	TAGATATGGA	TCCCGACTTC	AACGATATTG	TTAGCGAYAA	GGCGATAATC	AGCTCAAGAA	4920
	GGGACTGGGT	ATTYGAGTAC	AATGCAGCRG	CCTTTTGGA	GAAATACRGT	GARCGGTTGG	4980
	AGAGGCCYCC	TGCCAGRTC	GGACCRTCAC	GRCTTGTA	TGCTCTRATC	GATGGACGCT	5040
20	TAGAYAATAT	CCCAGCCCTG	CTAGAGCCAT	TTACAGGGG	AGCGGTTGAG	TTYGAGGATC	5100
	GGYTGACTGT	GCTCGTGCC	AAGGAGAARG	AGTTRAAGGT	AAAGGGAAGG	TTCTTCTCGA	5160
25	AGCAAACATT	GGCAATCAGG	ATATATCAGG	TTGTTGCTGA	AGCTGCACTT	AAGAAYGAGG	5220
	TTATGCCATA	CYTAAARACA	CAYTCAATGA	CCATGAGCTC	AACGGCYCTA	ACYCAYCTTC	5280
	TTAACCGGCT	ATCACATACT	ATCACTAAGG	GTGACTCCTT	TGTTATTAAC	YTWGAYTATA	5340
30	GYTCCTGGTG	CAACGGTTTC	CGACCAGAAC	TRCARGCCCC	AMTCTGTCGT	CAGTTGGATC	5400
	AGATGTTCAA	TTGCGGGTAC	TTCTTCAGGA	CTGGGTGCAC	ACTGCCATGC	TTTACCACGT	5460
35	TTATTATTCA	RGACAGRTTC	AACCGGCCCT	ATTCCYTCMG	TGGTGAGCCC	GTTGAAGACG	5520
	GWGTYACATG	CGCGGTTGGG	ACTAARACAA	TGGGRGAGGG	YATGAGGCAG	AAACTATGGA	5580
	CAATYCTTAC	GAGCTGCTGG	GAGATAATTG	CTCTTCGGGA	AATTAACGTG	ACGTTTAAYA	5640
40	TACTAGGCCA	RGGTGATAAT	CAGACAATCA	TYRTACATAA	ATCTGCAAGC	CAAAATAAYC	5700
	AGCTATTAGC	GGAGCGAGCA	YTRGGRGCYY	TGTACAAGCA	TGCTAGATTA	GCTGGCCATA	5760
45	ACCTYAAGGT	AGARGAATGY	TGGGTGTCAG	ATTGTCTGTA	TGAGTATGGA	AAGAAGCTYT	5820
	TCTTCCGTGG	TGTACCTGTC	CCRGGCTGTT	TGAAGCAGCT	CTCRCGGGTG	ACGGAYTCYA	5880
	CTGGRGAGYT	ATTCCCAAAC	CTATACTCAA	AGTTAGCCTG	CTTAACATCA	TCRTGYTTAA	5940
50	GCGCAGCGAT	GGCAGACACA	TCYCCATGGG	TGGCACTCGC	GACAGGTGTC	TGTCTGTATC	6000

	TTATCGAGTT RTATGTTGAG CTGCCTCCRG CAATCATGCA GGAYGAGTCG CTRTTTRACGA	6060
	CCCTCTGYCT CGTAGGYCCA TCCATTGGTG GGCTTCCRAC YCCTGCAACC CTRCCCAGTG	6120
5	TCTTTTTTCAG AGGAATGTCC GACCCAYTGC CCTTTCAGCT AGCACTCTTG CAGACCCTCA	6180
	TTAARACGAC AGGGGTGACY TGTAGCTTGG TGAATCGTGT GGTYAAGTTA CGGATAGCAC	6240
	CCTATCCAGA CTGGCTCTCY CTAGTGA CTG ACCCGACYTC ACTCAACATT GCYCARGTGT	6300
10	ACCGGCCAGA ACGTCARATC AGGAGGTGGA TTGAGGARGC RATAGCRACA AGCTCACACT	6360
	CGTCACGCAT AGCAACTTTY TTCCAGCAGS CCCTCACGGA GATGGCYCAG YTGCTTGCGA	6420
15	GGGACCTYTC AACAAATGATG CCTCTTCGRC CCCGGGATAT GTCGGCCTTA TTCGCATTAT	6480
	CAAATGTGCG ATAYGGTYTA AGCATTATAG ATCTATTTC AARTCCTCT ACCGTTGTYT	6540
	CTGCAAGTCA AGCTGTCCAT ATCGARGATG TTGCCCTAGA GAGTGTAAAG TATAAGGAAT	6600
20	CTATCATYCA GGGTCTGTTA GACACYACTG AGGGGTAYAA CATGCAACCT TATTTGGAAG	6660
	GTTGCACTTA CCTTGCAGCC AARCAGYTAC GKAGGTTGAC RTGGGGTCGA GACCTAGTTG	6720
25	GAGTYACAAT GCCGTTTGTT GCCGAGCAAT TCCATCCYCA YAGTTCTGTS GGTGCAAARG	6780
	CRGAACTCTA CCTCGAYGCT ATYATATACT GCCCACARGA GACRTTGCGG TCACACCATC	6840
	TGACTACCAG GGGGGACCAG CCGCTTTACC TYGGATCYAA TACGGCTGTC AMGGTYCAGC	6900
30	GAGGTGAGAT CACRGGCCTA ACAAAGTCAA GGGCTGCAA TCTAGTCARG GAGACTCTCG	6960
	TTCTCCAYCA GTGGTAYAAR GTCCGTAARG TTACCGATCC AACTTGAAC ACYCTCATGG	7020
35	CRCGCTTCTT RCTTGAGAAG GGRTACACAT CTGACGCTCG RCCTAGCATY CAGGGTGGGA	7080
	CCCTCACRCA TCGTCTCCCA TCCGYGGAG ACTCACGSCA RGGGCTYACT GGTATGTRA	7140
	ATATACTMAG YACGTGGCTY CGRTTCTCAA GTGATTATCT TCACTCTTTC TCGAAATCAT	7200
40	CAGAYGACTA YACAATCCAC TTYCAGCATG TATTCACATA CGGTTGCCTC TATGCTGATT	7260
	CGGTGATTAG ATCGGGCGGT GTTATTTCCT CTCCTTACCT TTTGAGTGCA AGTTGTAAAA	7320
45	CATGCTTTGA GAAGATAGAC TCAGAGGAGK TCGTCCTGGC ATGYGAACCY CAATAYAGGG	7380
	GTGCTGAGTG GCTGATATCA AAGCCAGTYA CTGTCCCTGA GCAGATAAYT GAYGCTGAAG	7440
	TCGAGTTTGA CCCCTGTGTG AGTGCGRGT ATTGTCTCGG GATTCTCATT GGCAAGTCAT	7500
50	TCTTRGTTGA CATAAGGGCA AGTGGGCATG ATATYATGGA GCAGCGGACA TGGGCTAACY	7560

	TGGAGAGGTT TTCTGTRTCG GACATGCAGA AACTTC CRTG GAGTATTGTA ATTCGGTCTC	7620
	TCTGGAGATT CCTTATTGGC GCACGRCTCC TYCAGTTTGA GAAGGCTGGC CTYATTAGRA	7680
5	TGCTGTATGC TGCRA CAGGT CCAACCCYYTA GCTTCCTAAT GAAAGTYTTT CAAGACTCAG	7740
	CCCTMCTYAT GGA CTGCGCA CCYCTYGATC GGCTGTMCCC TAGGATCAAC TTT CATAGTC	7800
	GGGGAGACCT CGTYG CYAAG CTYGT TTTTAT TRCCCTTCAT CAACCCGGGT ATAGTGGAGA	7860
10	TTGAAGTGTC TRGAATTAAT AGCAAGTAYC ATGCAGTATC GGAGGCYAAT ATGGATCTGT	7920
	ACATCGCTGC TGCMAARTCT GTGGGCGTRA AGCCACACACA GTTTGTTGAG GAAACAAACG	7980
15	ACTTTACGGC CCGCGGCCAC CACCATGGTT GTTATTCCCT TTCTTGGTCT AAGTCACGCA	8040
	ATCAATCACA GGTCTCTAAAG ATGGTAGTRC GGAAGCTGAA GCTMTGTGTC CTGTATATAT	8100
	ACCCACAGT CGATCCCGCC GTTGCTCTCG ACCTGTGCCA YTRCCAGCA YTA ACTATAA	8160
20	TCCTAGTGCT CGGCGGTGAC CCAGCGTACT AYGAGCGATT ACTTGAGATG GACCTR TGCG	8220
	GGGCTGTGTC AAGTCGMGTY GATATCCCCC ATTCYCTRGC TGSCAGAACG CACAGGGGGT	8280
25	TCRCARTRGG CCCAGACGCT GGTCCAGGTG TRATTAGACT YGACARGTTA GAGTCRGTTT	8340
	GTTAYGCYCA CCCCTGTTTR GAGGARCTAG AGTTTAATGC RTAYCTAGAC TCTGAGTTRG	8400
	TTGAYATTAG TGATATGTGC TGCCTCCCCY TAGCGACACC CTGTAAGGCC CTWTT CAGGC	8460
30	CARTRTATCG GAGCTTACAG TCGTTCAGGT TAGCCTTAAT GGACAACTAT AGTTTTGTMA	8520
	TGGACCTCAT TAYGATCCGR GGRSTGGACA TYAGGCCTCA CCTTGAGGAR TTTGAYGARC	8580
35	TGCTTGTGGT RGGRCAGCAY ATCCTCGGYC AGCCCGTCCT AGTRGAGGTT GTTTACTACG	8640
	TTGGAGTTGT TRGGAAGCGY CCTGTGTTAG CGAGGCATCC STGGTCAGCA GATCTTAAGC	8700
	GAATYACTGT RGGGGGGCGR GCKCCCTGCC CYTCTGCTGC YRGAYTGCGT GATGAGGATT	8760
40	GTCRGGGGTC TCTGYTGGTT GGGCTTCCYG CTGGRTTGAC GCAGTTRTTG RTRRTTGATT	8820
	RAGR TYRAGC CAYCTACTRC CCTATTCTTA AAAAACCATA YGTCAGTGGT GCAGTGCTTG	8880
45	GGYTTGGTTG TTGCTTTGTT GTAGCGCKTT	8910

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 603 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCAACGC	GACCATCGAG	TCTGGTCGAC	TCCCTGGAGG	ACGAAGAAGA	TCCCCAGACA	60
CTACGACGGG	AACGACCGGG	GTCAACCAAGA	CCACGGAAGG	TCCCAAGGAA	TGCATTGACC	120
CAACCAGTAG	ACCAGCTCCT	GAAGGACCTC	AGGAAGAACC	CCTCCATGAT	CTCAGACCCA	180
GACCAGCGAA	CCGGAAGGGA	GCAGCTGTCT	AATGATGAGC	TAATCAAGAA	GTTAGTGACG	240
GAGCTGGCCG	AGAATAGCAT	GATCGAGGCT	GAGGAGGTGC	GGGGCACTCT	TGGAGACATC	300
TCGGCTCGTA	TCGAGGCAGG	GTTTGAGTCC	CTGTCCGCCC	TCCAAGTGGA	AACCATCCAG	360
ACAGCTCAGC	GGTGCGATCA	CTCCGACAGC	ATCAGGATCC	TCGGCGAGAA	CATCAAGATA	420
CTAGATCGCT	CCATGAAGAC	AATGATGGAG	ACAATGAAGC	TCATGATGGA	GAAGGTGGAT	480
CTCCTCTACG	CATCAACCGC	CGTTGGGACC	TCTGCACCCA	TGTTGCCCTC	CCATCCTGCA	540
CCTCCGCGCA	TTTATCCCCA	GCTCCCAAGT	GCCCCGACAA	CGGATGAATG	GGACATCATA	600
CCA						603

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 603 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	ATGGCAACGG AACCATCGAG TCTGGTCGAC TCCCTGGAGG ACGAAGAAGA TCCCCAGACA	60
5	CTACGACGGG AACGATCGGG GTCACCAAGA CCACGGAAGG TCCCAAGGAA TGCATTGACC	120
	CAACCAGTAG ACCAGCTCCT GAAGGACCTC AGGAAGAACC CCTCCATGAT CTCAGACCCA	180
	GACCAGCGAA CCGGAAGGGA GCAGCTGTCT AATGATGAGC TAATCAAGAA GTTAGTGACG	240
10	GAGCTGGCCG AGAATAGCAT GATCGAGGCT GAGGAGGTGC GGGGCACTCT TGGAGACATC	300
	TCGGCTCGTA TCGAGGCAGG GTTTGAGTCC CTGTCCGCCC TCCAAGTGA AACCATCCAG	360
15	ACAGCTCAGC GGTGCGATTA CTCCGACAGC ATCAGGATCC TCGGCGAGAA CATCAAGATA	420
	CTAGATCGCT CCATGAAGAC AATGATGGAG ACAATGAAGC TCATGATGGA GAAGGTGGAT	480
	CTCCTCTACG CATCAACCGC CGTTGGGACC TCTGCACCCA TGTTCGCCCTC CCATCCTGCA	540
20	CCTCCGCGCA TTTATCCCCA GCTCCCAAGT GCCCCGACAA CGGATGAGTG GGACATCATA	600
	CCA	603

25 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 603 base pairs
	(B) TYPE: nucleic acid
30	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	ATGGCAACGG GACCATCGAG TCTGGTCGAC TCCCTGGAGG ACGAAGAAGA TCCCCAGACA	60
45	CTACGACGGG AACGATCGGG GTCACCAAGA CCACGGAAGG TCCCAAGGAA TGCATTGACC	120
	CAACCAGTAG ACCAGCTCCT GAAGGACCTC AGGAAGAACC CCTCCATGAT CTCAGACCCA	180
	GACCAGCGAA CCGGAAGGGA GCAGCTGTCT AATGATGAGC TAATCAAGAA GTTAGTGACG	240
50	GAGCTGGCCG AGAATAGCAT GATCGAGGCT GAGGAGGTGC GGGGCACTCT TGGAGACATC	300

	TCGGCTCGTA TCGAGGCAGG GTTTGAGTCC CTGTCCGCCC TCCAAGTGGA AACCATCCAG	360
	ACAGCTCAGC GGTGCGATCA CTCCGACAGC ATCAGGATCC TCGGCGAGAA CATCAAGATA	420
5	CTAGATCGCT CCATGAAGAC AATGATGGAG ACAATGAAGC TCATGATGGA GAAGGTGGAT	480
	CTCCTCTACG CATCAACCGC CGTTGGGACC TCTGCACCCA TGTTGCCCTC CCATCCTGCA	540
	CCTCCGCGCA TTTATCCCCA GCTCCCAAGT GCCCCGACAA CGGATGAGTG GGACATCATA	600
10	CCA	603

(2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 603 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

25 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

30	ATGGCAACGG AACCATCGAG TCTGGTCGAC TCCCTGGAGG ACGAAGAAGA TCCCCAGACA	60
	CTACGA <sup>1</sup> CGGG AACGATCGGG GTCACCAAGA CCACGGAAGG TCCCAAGGAA TGCATTGACC	120
35	CAACCAGTAG ACCAGCTCCT GAAGGACCTC AGGAAGAACC CCTCCATGAT CTCAGACCCA	180
	GACCAGCGAA CCGGAAGGGA GCAGCTGTCT AATGATGAGC TAATCAAGAA GTTAGTGACG	240
	GAGCTGGCCG AGAATAGCAT GATCGAGGCT GAGGAGGTGC GGGGCACTCT TGGAGACATC	300
40	TCGGCTCGTA TCGAGGCAGG GTTTGAGTCC CTGTCCGCCC TCCAAGTGGA AACCATCCAG	360
	ACAGCTCAGC GGTGCGACCA CTCCGACAGC ATCAGGATCC TCGGCGAGAA CATCAAGATA	420
45	CTAGATCGCT CCATGAAGAC AATGATGGAG ACAATGAAGC TCATGATGGA GAAGGTGGAT	480
	CTCCTCTACG CATCAACCGC CGTTGGGACC TCTGCACCCA TGTTGCCCTC CCATCCTGCA	540
	CCTCCGCGCA TTTATCCCCA GCTCCCAAGT GCCCCGACAA CGGATGAGTG GGACATCATA	600
50	CCA	603

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAATTCAA AACATTCTTA TGTGGAGCTC AAGGACAAGG TAATCGTCCC TGGATGGCCC	60
ACACTGATGC TTGAGATAGA CTTTGTAGGG GGGACTTCAC GGAACCAGTT CCTTAACATC	120
CCATTCTTTT CAGTGAAAGA GCCTCTGCAG CTTCCACGCG AGAAGAAGTT GACCGACTAC	180
TTTACTATTG ACGTAGAACC AGCAGGTCAT TCCCTGGTCA ATATATACTT CCAGATTGAC	240
GACTTCTTGC TCCTAACACT CAACTCACTA TCTGTGTACA AGGACCCGAT TAGAAAATAC	300
ATGTTCTTAC GCCTCAACAA GGACCAGAGC AAGCACGCAA TCAATGCAGC CTTCAATGTC	360
TTTTCTTATC GGCTTCGGAA CATTGGTGTT GGTCTCTCTG GCCCGGACAT TCGATCTTCA	420
GGGCCT	426

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAATTCAA AGCATTTCCTA TGTGGAGCTC AAGGACAAGG TAATCGTCCC TGGATGGCCC 60  
 AACTGATGC TTGAGATAGA CTTTGTAGGG GGGACTTCAC GGAACCAGTT CCTTAACATC 120  
 5 CCATTCTTT CAGTGAAAGA GCCTCTGCAG CTTCCACGCG AGAAGAAGTT GACCGACTAC 180  
 TTTACTATTG ACGTAGAACC AGCAGGTCAT TCCCTGGTCA ATATATACTT TCAGATTGAC 240  
 GACTTCTTGC TCCTAACACT CAACTCACTA TCTGTGTACA AGGACCCGAT TAGAAAATAC 300  
 10 ATGTTCTTAC GCCTCAACAA GGACCAGAGC AAGCACGCAA TCAATGCAGC CTTCAATGTC 360  
 TTTTCTTATC GGCTTCGGAA CATTGGTGTT GGTCTCTCTG GCCCGGACAT TCGATCTTCA 420  
 15 GGGCCT 426

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 426 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

35 ATGAATTCAA *AGCATTTCCTA* TGTGGAGCTC AAGGACAAGG TAATCGTCCC TGGATGGCCC 60  
 AACTGATGC TTGAGATAGA CTTTGTAGGG GGGACTTCAC GGAACCAGTT CCTTAACATC 120  
 CCATTCTTT CAGTGAAAGA GCCTCTGCAG CTTCCACGCG AGAAGAAGTT GACCGACTAC 180  
 40 TTTACTATTG ACGTAGAACC AGCAGGTCAT TCCCTGGTCA ATATATACTT CCAGATTGAC 240  
 GACTTCTTGC TCCTAACACT CAACTCACTA TCTGTGTACA AGGACCCGAT TAGAAAATAC 300  
 45 ATGTTCTTAC GCCTCAACAA GGACCAGAGC AAGCACGCAA TCAATGCAGC CTTCAATGTC 360  
 TTTTCTTATC GGCTTCGGAA CATTGGTGTT GGTCTCTCTG GCCCGGACAT TCGATCTTCA 420  
 GGGCCT 426

50 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCAA AGCATTCTTA TGTGGAGCTC AAGGACAAGG TAATCGTCCC TGGATGGCCC 60  
ACACTGATGC TTGAGATAGG CTTTGTAGGG GGGACTTCAC GGAACCAGTT CCTTAACATC 120  
CCATTTCTTT CAGTGAAAGA GCCTCTGCAG CTTCACGCG AGAAGAAGTT GACCGACTAC 180  
TTTACTATTG ACGTAGAACC AGCAGGTCAT TCCCTGGTCA ATATATACTT CCAGATTGAC 240  
GACTTCTTGC TCCTAACACT CAACTCACTA TCTGTGTACA AGGACCCGAT TAGAAAATAC 300  
ATGTTCTTAC GCCTCAACAA GGACCAGAGC AAGCACGCAA TCAATGCAGC CTTCAATGTC 360  
TTTTCTTATC GGCTTCGGAA CATTGGTGTT GGTCTCTCG GCCCGGACAT TCGATCTTCA 420  
GGGCCT 426

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1521 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGCAGCCTT CAATGTCTTT TCTTATCGGC TTCGGAACAT TGGTGTTGGT CCTCTCGGCC 60

	CGGACATTCG ATCTTCAGGG CCTTAGCTGC AATACTGACT CCACTCCTGG ACTGATTGAC	120
	CTGGAGATAA GCGGACTTTG CCACACCCCA ACGGAAAATG TCATTTTCATG CGAGGTTAGT	180
5	TATCTCAACC ACACGACTAT TAGCCTCCCG GCAGTCCACA CATCATGCCT CAAGTACCAC	240
	TGCAAAACCT ATTGGGGATT CTTTGGTAGC TACAGCGCTG ACCGAATCAT AAATCGGTAC	300
	ACTGGTACTG TTAAGGGTTG TCTAAACAAC TCAGCACCAG AGGACCCCTT CGAGTGCAAC	360
10	TGGTTCTACT GCTGCTCGGC GATTACAACA GAGATCTGCC GATGCTCTAT TACAAATGTC	420
	ACGGTGGCTG TGCAAACATT CCCACCGTTC ATGTACTGCA GTTTTGCAGA CTGCAGTACC	480
15	GTGAGCCAAC AGGAGCTAGA GAGTGGAAAG GCAATGCTGA GCGATGGCAG TACATTAAC	540
	TATACCCCGT ATATCCTACA GTCAGAAAGT GTGAACAAAA CCCTCAATGG GACCATACTC	600
	TGCAACTCAT CCTCTAAGAT AGTTTCCTTC GATGAATTTA GGCCTTCATA CTCCCTAACG	660
20	AATGGTAGTT ACCAGAGCTC ATCAATCAAT GTGACGTGTG CAAACTACAC GTCGTCCTGC	720
	CGGCCCAGGT TGAAAAGGCG GCGTAGGGAC ACCCAGCAGA TTGAGTATCT AGTTCACAAG	780
25	CTTAGGCCCCA CACTGAAAGA TGCATGGGAG GACTGTGAGA TCCTCCAGTC TCTGCTCCTA	840
	GGGGTGTTTG GTACTGGGAT CGCAAGTGCT TCTCAATTTT TGAGGAGCTG GCTCAACCAC	900
	CCTGACATCA TCGGGTATAT AGTTAATGGA GTTGGGGTTG TCTGGCAATG CCATCGTGTT	960
30	AATGTCACGT TCATGGCGTG GAATGAGTCC ACCTATTACC CTCCAGTAGA TTACAATGGG	1020
	CGGAAGTACT TCCTGAATGA TGAGGGAAGG TTACAAACAA ACACCCCCGA GGCAAGGCCA	1080
35	GGGCTTAAGC GGGTCATGTG GTTCGGCAGG TACTTCCTAG GGACAGTAGG GTCTGGGGTG	1140
	AAACCGAGGA GGATTCGCTA CAATAAGACC TCACATGACT ACCACCTGGA GGAGTTTGAG	1200
	GCAAGTCTCA ACATGACCCC TCAGACCACT ATCGCCTCGG GTCATGAGAC AGACCGCATA	1260
40	AATCATGCCT ACGGAACGCA GGCTGATCTC CTTCCATACA CCAGGTCTAG TAATATAACA	1320
	TCTACGGATA CAGGCTCAGG CTGGGTGCAC ATCGGCCTAC CCTCATTTGC TTTCTCAAT	1380
45	CCCCTCGGGT GGCTCAGGGA CCTACTTGCA TGGGCAGCCT GGTGGGTGG GGTTCATAC	1440
	TTAATAAGTC TTTGTGTTTC CTTACCAGCC TCCTTCGCGA GGAGGAGACG CCTCGGCCGG	1500
	TGGCAGGAAT AAACCGTACC G	1521

50

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGCAGCCTT	CAATGTCTTT	TCTTATCGGC	TCGGAACAT	TGGTGTGGT	CCTCTCGGCC	60
CGGACATTCG	ATCTTCAGGG	CCTTAGCTGC	AATACTGACT	CCACTCCTGG	ACTGATTGAC	120
CTGGAGATAA	GGCGACTTTG	CCACACCCCA	ACGGAAAATG	TCATTTCATG	CGAGGTTAGT	180
TATCTCAACC	ACACGACTAT	TAGCCTCCCG	GCAGTCCACA	CATCATGCCT	CAAGTACCAC	240
TGCAAAACCT	ATTGGGGATT	CTTTGGTAGC	TACAGCGCTG	ACCGAATCAT	AAATCGGTAC	300
ACTGGTACTG	TTAAGGGTTG	TCTAAACAAC	TCAGCACCAG	AGGACCCCTT	CGAGTGCAAC	360
TGGTTCTACT	GCTGCTCGGC	GATTACAACA	GAGATCTGCC	GATGCTCTAT	TACAAATGTC	420
ACGGTGGCTG	TGCAAAACATT	CCCACCGTTC	ATGTA CTGCA	GTTTTCGAGA	CTGCAGTACC	480
GTGAGCCAAC	AGGAGCTAGA	GAGTGGAAAAG	GCAATGCTGA	GCGATGGCAG	TACATTA ACT	540
TATACCCCGT	ATATCCTACA	GTCAGAAAGTC	GTGAACAAAA	CCCTCAATGG	GACCATACTC	600
TGCAACTCAT	CCTCTAAGAT	AGTTTCCTTC	GATGAATTTA	GGCGTTCATA	CTCCCTAACG	660
AATGGTAGTT	ACCAGAGCTC	ATCAATCAAT	GTGACGTGTG	CAA ACTACAC	GTGCTCCTGC	720
CGGCCCAGGT	TGAAAAGGCG	GCGTAGGGAC	ACCCAGCAGA	TTGAGTATCT	AGTTCACAAG	780
CTTAGGCCCA	CACTGAAAGA	TGCATGGGAG	GACTGTGAGA	TCCTCCAGTC	TCTGCTCCTA	840
GGGGTGTTTG	GTA CTGGGAT	CGCAAGTGCT	TCTCAATTTT	TGAGGAGCTG	GCTCAACCAC	900
CCTGACATCA	TCGGGTATAT	AGTTAATGGA	GTTGGGGTTG	TCTGGCAATG	CCATCGTGTT	960
AATGTCACGT	TCATGACGTG	GAATGAGTCC	ACCTATTACC	CTCCAGTAGA	TTACAATGGG	1020
CGGAAGTACT	TCCTGAATGA	TGAGGGAAGG	TTACAAACAA	ACACCCCCGA	GGCAAGGCCA	1080

	GGGCTTAAGC GGGTCATGTG GTTCGGCAGG TACTTCCTAG GGACAGTAGG GTCTGGGGTG	1140
	AAACCGAGGA GGATTCGGTA CAATAAGACC TCACATGACT ACCACCTGGA GGAGTTTGAG	1200
5	GCAAGTCTCA ACATGACCCC TCAGACCACT ATCACCTCGG GTCATGAGAC AGACCCCATATA	1260
	AATCATGCCT ACGGAACGCA GGCTGATCTC CTTCCATACA CCAGGTCTAG TAATATAACA	1320
	TCTACGGATA CAGGCTCAGG CTGGGTGCAC ATCGGCCTAC CCTCATTTGC TTTCTCAAT	1380
10	CCCCTCGGGT GGCTCAGGGA CCTACTTGCA TGGGCAGCCT GGTGGGTGG GGTCTATAC	1440
	TTAATAAGTC TTTGTGTTTC CTTACCAGCC TCCTTCGCGA GGAGGAGACG CCTCGGCCCG	1500
15	TTGCAGGAAT AAACCGTACC G	1521

(2) INFORMATION FOR SEQ ID NO:12:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 1521 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

25	(ii) MOLECULE TYPE: cDNA
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	(iii) HYPOTHETICAL: NO
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30	(iv) ANTI-SENSE: NO
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

35	ATGCAGCCTT CAATGTCTTT TCTTATCGGC TTCGGAACAT TGGTGTTGGT CCTCTCGGCC	60
	CGGACATTCG ATCTTCAGGG CCTTAGCTGC AATACTGACT CCACTCCTGG ACTGATTGAC	120
	CTGGAGATAA GGCGACTTTG CCACACCCCA ACGGAAAATG TCATTTTCATG CGAGGTAGT	180
40	TATCTCAACC ACACGACTAT TAGCCTCCCG GCAGTCCACA CATCATGCCT CAAGTACCAC	240
	TGCAAAACCT ATTGGGGATT CTTTGGTAGC TACAGCGCTG ACCGAATCAT AAATCGGTAC	300
45	ACTGCTACTG TTAAGGGTTG TCTAAACAAC TCAGCACCAG AGGACCCCTT CGAGTGCAAC	360
	TGTTTCTACT GCTGCTCGGC GATTACAACA GAGATCTGCC GATGCTCTAT TACAAATGTC	420
	ACGGTGGCTG TGCAACATT CCCACCGTTC ATGTACTGCA GTTTTGCAGA CTGCAGTACC	480
50	GTGAGCCAAC AGGAGCTAGA GAGTGGAAG GCAATGCTGA GCGATGGCAG TACATTAAC	540



TATACCCCGT ATATCCTACA GTCAGAAGTC GTGAACAAAA CCCTCAATGG GACCATACTC 600  
 TGCAACTCAT CCTCTAAGAT AGTTTCCTTC GATGAATTTA GGCGTTCATA CTCCCTAACG 660  
 5 AATGGTAGTT ACCAGAGCTC ATCAATCAAT GTGACGTGTG CAAACTACAC GTCGTCCTGC 720  
 CGGCCCAGGT TGAAAAGGCG GCGTAGGGAC ACCCAGCAGA TTGAGTATCT AGTTCACAAG 780  
 CTTAGGCCCA CACTGAAAGA TGCATGGGAG GACTGTGAGA TCCTCCAGTC TCTGCTCCTA 840  
 10 GGGGTGTTTG GTACTGGGAT CGCAAGTGCT TCTCAATTTT TGAGGAGCTG GCTCAACCAC 900  
 CCTGACATCA TCGGGTATAT AGTTAATGGA GTTGGGGTTG TCTGGCAATG CCATCGTGTT 960  
 15 AATGTCACGT TCATGACGTG GAATGAGTCC ACCTATTACC CTCCAGTAGA TTACAATGGG 1020  
 CGGAAGTACT TCCTGAATGA TGAGGGAAGG TTACAAACAA ACACCCCCGA GGCAAGGCCA 1080  
 GGGCTTAAGC GGGTCATGTG GTTCGGCAGG TACTTCCTAG GGACAGTAGG GTCTGGGGTG 1140  
 20 AAACCGAGGA GGATTCGGTA CAATAAGACC TCACATGACT ACCACCTGGA GGAGTTTGAG 1200  
 GCAAGTCTCA ACATGACCCC TCAGACCAGT ATCGCCTCGG GTCATGAGAC AGACCCCATATA 1260  
 25 AATCATGCCT ACGGAACGCA GGCTGATCTC CTTCCATACA CCAGGTCTAG TAATATAACA 1320  
 TCTACGGATA CAGGCTCAGG CTGGGTGCAC ATCGGCCTAC CCTCATTTCG TTTCTCAAT 1380  
 CCCCTCGGGT GGCTCAGGGA CCTACTTGCA TGGGCAGCCT GGTGTTGGTG GGTTCCTATAC 1440  
 30 TTAATAAGTC TTTGTGTTTC CTTACCAGCC TCCTTCGCGA GGAGGAGACG CCTCGGCCGG 1500  
 TGGCAGGAAT AAACCGTACC G 1521

35 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 571 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5    TTCAYACAGT AACGCCYAGC CTTGTGTTTC TATGTTTGCT AATCCCAGGA CTGCACGCTG    60  
      CGTTTGTTC ACGAGGGGTG CCTCGTGAAT CYTACCTGTC GACGCCTRTY ACGCGTGGRG    120  
 10    AACAGACTGT YGTTAAGACT GCRRAGTTTT ACGGGGAAAA GACRACRCAG CGTGATCTCA    180  
      CCGAGCTGGA GATCTCCTCT ATMTTCAGCC ATTGTTGCTC ATTACTAATW GGGGTTGTGA    240  
      TAGGATCGTC RTCTAAGATY AAAGCAGRAG CCGAGCAGAT CAAGAAAAGG TTAAAACTA    300  
 15    TGATGGCAGC CKTAAACCGG CCATCCCATG GTGAGACTGC TACTACTY CAGATGTTTA    360  
      ATCCACATGA GGCTATAGAT TGGATTAACG GCCARCCCTG GGTAGGCTCC TTTGTGTTGY    420  
      CTCTACTAAC TACAGACTTT GAGTCCCCAG GTAAAGAATT YATGGAYCAG ATTAARCTTG    480  
      TCGCAAGTTA TGCRCAGATG ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGYA    540  
 20    TGGATGCTAC CTTACAATC CCYGTAGTTG C    571

(2) INFORMATION FOR SEQ ID NO:14:

25    (i) SEQUENCE CHARACTERISTICS:  
      (A) LENGTH: 571 base pairs  
      (B) TYPE: nucleic acid  
      (C) STRANDEDNESS: single  
      (D) TOPOLOGY: linear

30    (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40    TTCATACAGT AACGCCCAGC CTTGTGTTTC TATGTTTGCT AATCCCAGGA CTGCACGCTG    60  
      CGTTTGTTC ACGAGGGGTG CCTCGTGAAT CCTACCTGTC GACGCCTGTC ACGCGTGAG    120  
      AACAGACTGT TGTTAAGACT GCGAAGTTTT ACGGGGAAAA GACGACGCAG CGTGATCTCA    180  
 45    CCGAGCTGGA GATCTCCTCT ATCTTCAGCC ATTGTTGCTC ATTACTAATA GGGGTTGTGA    240  
      TAGGATCGTC GTCTAAGATC AAAGCAGGAG CCGAGCAGAT CAAGAAAAGG TTAAAACTA    300  
      TGATGGCAGC CTTAAACCGG CCATCCCATG GTGAGACTGC TACTACTC CAGATGTTTA    360  
 50    ATCCACATGA GGCTATAGAT TGGATTAACG GCCAACCTG GGTAGGCTCC TTTGTGTTGC    420

CTCTACTAAC TACAGACTTT GAGTCCCCAG GTAAAGAATT TATGGACCAG ATTAAGCTTG 480  
TCGCAAGTTA TGCACAGATG ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGCA 540  
5 TGGATGCTAC CCTTACAATC CCTGTAGTTG C 571

(2) INFORMATION FOR SEQ ID NO:15:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 571 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

25 TTCATACAGT AACGCCCAGC CTTGTGTTTC TATGTTTGCT AATCCCAGGA CTGCACGCTG 60  
CGTTTGTTC ACGAGGGGTG CCTCGTGAAT CCTACCTGTC GACGCCTATC ACGCGTGGAG 120  
AACAGACTGT TGTTAAGACT GCGGAGTTTT ACGGGGAAAA GACGACGCAG CGTGATCTCA 180  
30 CCGAGCTGGA GATCTCCTCT ATCTTCAGCC ATTGTTGCTC ATTACTAATA GGGGTTGTGA 240  
TAGGATCGTC GTCTAAGATC AAAGCAGAAG CCGAGCAGAT CAAGAAAAGG TTTAAAACTA 300  
35 TGATGGCAGC CGTAAACCGG CCATCCCATG GTGAGACTGC TACACTACTC CAGATGTTTA 360  
ATCCACATGA GGCTATAGAT TGGATTAACG GCCAACCCTG GGTAGGCTCC TTTGTGTTGT 420  
CTCTACTAAC TACAGACTTT GAGTCCCCAG GTAAAGAATT TATGGACCAG ATTAAGCTTG 480  
40 TCGCAAGTTA TGCACAGATG ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGCA 540  
TGGATGCTAC CCTTACAATC CCTGTAGTTG C 571

45 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 571 base pairs  
50 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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10 TTCATACAGT AACGCCCAGC CTTGTGTTTC TATGTTTGCT AATCCCAGGA CTGCACGCTG      60
   CGTTTGTTCA CGGAGGGGTG CCTCGTGAAT CCTACCTGTC GACGCCTATC ACGCGTGGAG      120
15 AACAGACTGT TGTTAAGACT GCGAAGTTTT ACGGGGAAAA GACGACGCAG CGTGATCTCA      180
   CCGAGCTGGA GATCTCCTCT ATCTTCAGCC ATTGTTGCTC ATTACTAATA GGGGTTGTGA      240
   TAGGATCGTC GTCTAAGATC AAAGCAGGAG CCGAGCAGAT CAAGAAAAGG TTAAAACTA      300
20 TGATGGCAGC CTTAAACCGG CCATCCCATG GTGAGACTGC TACACTACTC CAGATGTTTA      360
   ATCCACATGA GGCTATAGAT TGGATTAAAG GCCAACCCCTG GGTAGGCTCC TTTGTGTTGT      420
25 CTCTACTAAC TACAGACTTT GAGTCCCCAG GTAAAGAATT TATGGACCAG ATTAAGCTTG      480
   TCGCAAGTTA TGCACAGATG ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGCA      540
   TGGATGCTAC CCTTACAATC CCTGTAGTTG C      571

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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50 TGACCATGAG CTCAACGGCY CTAACYCAYC TTCTTAACCG GCTATGACAT ACTATCACTA      60
   AGGGTGACTC CTTTGTTATT AACYTWGAYT ATAGYTCCTG GTGCAACGGT TTCCGACCAG      120

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	AACTRCARGC CCCAMTCTGT CGTCAGTTGG ATCAGATGTT CAATTGCGGG TACTTCTTCA	180
	GGACTGGGTG CACACTGCCA TGCTTTACCA CGTTTATTAT TCARGACAGR TTCAACCCGC	240
5	CCTATTCCYT CMGTGGTGAG CCCGTTGAAG ACGGWGTYAC ATGCGCGGTT GGGACTAARA	300
	CAATGGGRGA GGGYATGAGG CAGAAACTAT GGACAATYCT TACGAGCTGC TGGGAGATAA	360
	TTGCTCTTCG GGAAATTAAC GTGACGTTTA AYATACTAGG CCARGGTGAT AATCAGACAA	420
10	TCATYRTACA TAAATCTGCA AGCCAAAATA AYCAGCTATT AGCGGAGCGA GCAYTRGGRG	480
	CYYTGTAACA GCATGCTAGA TTAGCTGGCC ATAACCTYAA GGTAGARGAA TGYTGGGTGT	540
15	CAGATTGTCT GTATGAGTAT GGAAAGAAGC TYTTCTTCCG TGGTGTACCT GTCCCRGGCT	600
	GTTTGAAGCA GCTCTCRCGG GTGACGGAYT CYACTGGRGA GYTATTCCCA AACCTATACT	660
	CAAAGTTAGC CTGCTWAACA TCATCRTGY	689

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 689 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

40	TGACCATGAG CTCAACGGCT CTAACCTACC TTCTTAACCG GCTATCACAT ACTATCACTA	60
	AGGGTGACTC CTTTGTTATT AACCTTGAAG ATAGTTCTCTG GTGCAACGGT TTCCGACCAG	120
	AACTGCAGGC CCCAATCTGT CGTCAGTTGG ATCAGATGTT CAATTGCGGG TACTTCTTCA	180
45	GGACTGGGTG CACACTGCCA TGCTTTACCA CGTTTATTAT TCAAGACAGG TTCAACCCGC	240
	CCTATTCCCT CAGTGGTGAG CCCGTTGAAG ACGGAGTTAC ATGCGCGGTT GGGACTAAAA	300
	CAATGGGGGA GGGCATGAGG CAGAAACTAT GGACAATCCT TACGAGCTGC TGGGAGATAA	360
50	TTGCTCTTCG GGAAATTAAC GTGACGTTTA ACATACTAGG CCAAGGTGAT AATCAGACAA	420

TCATCATACA TAAATCTGCA AGCCAAAATA ACCAGCTATT AGCGGAGCGA GCACTAGGGG 480  
 CCCTGTACAA GCATGCTAGA TTAGCTGGCC ATAACCTCAA GGTAGAGGAA TGCTGGGTGT 540  
 5 CAGATTGTCT GTATGAGTAT GGAAAGAAGC TTTTCTTCCG TGGTGTACCT GTCCCGGGCT 600  
 GTTTGAAGCA GCTCTCACGG GTGACGGATT CTA CTGGAGA GCTATTCCCA AACCTATACT 660  
 CAAAGTTAGC CTGCTTAACA TCATCATGC 689

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 689 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGACCATGAG CTCAACGGCT CTAATCACC TTCTTAACCG GCTATCACAT ACTATCACTA 60  
 30 AGGGTGACTC CTTTGTTATT AACCTTGACT ATAGTTCCTG GTGCAACGGT TTCCGACCAG 120  
 AACTGCAGGC CCCAATCTGT CGTCAGTTGG ATCAGATGTT CAATTGCGGG TACTTCTTCA 180  
 35 GGACTGGGTG CACACTGCCA TGCTTTACCA CGTTTATTAT TCAAGACAGG TTCAACCCGC 240  
 CCTATTCCCT CAGTGGTGAG CCCGTTGAAG ACGGAGTTAC ATGCGCGGTT GGGACTAAAA 300  
 CAATGGGGGA GGGCATGAGG CAGAAACTAT GGACAATCCT TACGAGCTGC TGGGAGATAA 360  
 40 TTGCTCTTCG GGAAATTAAC GTGACGTTTA ACATACTAGG CCAAGGTGAT AATCAGACAA 420  
 TCATCATACA TAAATCTGCA AGCCAAAATA ACCAGCTATT AGCGGAGCGA GCACTAGGGG 480  
 45 CCCTGTACAA GCATGCTAGA TTAGCTGGCC ATAACCTCAA GGTAGAGGAA TGCTGGGTGT 540  
 CAGATTGTCT GTATGAGTAT GGAAAGAAGC TTTTCTTCCG TGGTGTACCT GTCCCGGGCT 600  
 GTTTGAAGCA GCTCTCACGG GTGACGGATT CTA CTGGAGA GCTATTCCCA AACCTATACT 660  
 50 CAAAGTTAGC CTGCTAAACA TCATCATGC 689

(2) INFORMATION FOR SEQ ID NO:20:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

15 Met Ala Thr Glu Pro Ser Ser Leu Val Asp Ser Leu Glu Asp Glu Glu  
1 5 10 15

20 Asp Pro Gln Thr Leu Arg Arg Glu Arg Ser Gly Ser Pro Arg Pro Arg  
20 25 30

Lys Val Pro Arg Asn Ala Leu Thr Gln Pro Val Asp Gln Leu Leu Lys  
35 40 45

25 Asp Leu Arg Lys Asn Pro Ser Met Ile Ser Asp Pro Asp Gln Arg Thr  
50 55 60

Gly Arg Glu Gln Leu Ser Asn Asp Glu Leu Ile Lys Lys Leu Val Thr  
65 70 75 80

30 Glu Leu Ala Glu Asn Ser Met Ile Glu Ala Glu Glu Val Arg Gly Thr  
85 90 95

35 Leu Gly Asp Ile Ser Ala Arg Ile Glu Ala Gly Phe Glu Ser Leu Ser  
100 105 110

Ala Leu Gln Val Glu Thr Ile Gln Thr Ala Gln Arg Cys Asp Tyr Ser  
115 120 125

40 Asp Ser Ile Arg Ile Leu Gly Glu Asn Ile Lys Ile Leu Asp Arg Ser  
130 135 140

Met Lys Thr Met Met Glu Thr Met Lys Leu Met Met Glu Lys Val Asp  
145 150 155 160

45 Leu Leu Tyr Ala Ser Thr Ala Val Gly Thr Ser Ala Pro Met Leu Pro  
165 170 175

Ser His Pro Ala Pro Pro Arg Ile Tyr Pro Gln Leu Pro Ser Ala Pro  
50 180 185 190

Thr Thr Asp Glu Trp Asp Ile Ile Pro  
195 200

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala Thr Gly Pro Ser Ser Leu Val Asp Ser Leu Glu Asp Glu Glu  
1 5 10 15

Asp Pro Gln Thr Leu Arg Arg Glu Arg Ser Gly Ser Pro Arg Pro Arg  
20 25 30

Lys Val Pro Arg Asn Ala Leu Thr Gln Pro Val Asp Gln Leu Leu Lys  
35 40 45

Asp Leu Arg Lys Asn Pro Ser Met Ile Ser Asp Pro Asp Gln Arg Thr  
50 55 60

Gly Arg Glu Gln Leu Ser Asn Asp Glu Leu Ile Lys Lys Leu Val Thr  
65 70 75 80

Glu Leu Ala Glu Asn Ser Met Ile Glu Ala Glu Glu Val Arg Gly Thr  
85 90 95

Leu Gly Asp Ile Ser Ala Arg Ile Glu Ala Gly Phe Glu Ser Leu Ser  
100 105 110

Ala Leu Gln Val Glu Thr Ile Gln Thr Ala Gln Arg Cys Asp His Ser  
115 120 125

Asp Ser Ile Arg Ile Leu Gly Glu Asn Ile Lys Ile Leu Asp Arg Ser  
130 135 140

Met Lys Thr Met Met Glu Thr Met Lys Leu Met Met Glu Lys Val Asp  
145 150 155 160

Leu Leu Tyr Ala Ser Thr Ala Val Gly Thr Ser Ala Pro Met Leu Pro  
165 170 175

Ser His Pro Ala Pro Pro Arg Ile Tyr Pro Gln Leu Pro Ser Ala Pro  
180 185 190



Thr Thr Asp Glu Trp Asp Ile Ile Pro  
195 200

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Asn Ser Lys His Ser Tyr Val Glu Leu Lys Asp Lys Val Ile Val  
1 5 10 15

Pro Gly Trp Pro Thr Leu Met Leu Glu Ile Asp Phe Val Gly Gly Thr  
20 25 30

Ser Arg Asn Gln Phe Leu Asn Ile Pro Phe Leu Ser Val Lys Glu Pro  
35 40 45

Leu Gln Leu Pro Arg Glu Lys Lys Leu Thr Asp Tyr Phe Thr Ile Asp  
50 55 60

Val Glu Pro Ala Gly His Ser Leu Val Asn Ile Tyr Phe Gln Ile Asp  
65 70 75 80

Asp Phe Leu Leu Leu Thr Leu Asn Ser Leu Ser Val Tyr Lys Asp Pro  
85 90 95

Ile Arg Lys Tyr Met Phe Leu Arg Leu Asn Lys Asp Gln Ser Lys His  
100 105 110

Ala Ile Asn Ala Ala Phe Asn Val Phe Ser Tyr Arg Leu Arg Asn Ile  
115 120 125

Gly Val Gly Pro Leu Gly Pro Asp Ile Arg Ser Ser Gly Pro  
130 135 140

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

5	Met	Asn	Ser	Lys	His	Ser	Tyr	Val	Glu	Leu	Lys	Asp	Lys	Val	Ile	Val
	1			5					10						15	
	Pro	Gly	Trp	Pro	Thr	Leu	Met	Leu	Glu	Ile	Asp	Phe	Val	Gly	Gly	Thr
				20					25					30		
10	Ser	Arg	Asn	Gln	Phe	Leu	Asn	Ile	Pro	Phe	Leu	Ser	Val	Lys	Glu	Pro
			35				40						45			
	Leu	Gln	Leu	Pro	Arg	Glu	Lys	Lys	Leu	Thr	Asp	Tyr	Phe	Thr	Ile	Asp
15		50					55					60				
	Val	Glu	Pro	Ala	Gly	His	Ser	Leu	Val	Asn	Ile	Tyr	Phe	Gln	Ile	Asp
	65				70					75					80	
20	Asp	Phe	Leu	Leu	Leu	Thr	Leu	Asn	Ser	Leu	Ser	Val	Tyr	Lys	Asp	Pro
				85					90						95	
	Ile	Arg	Lys	Tyr	Met	Phe	Leu	Arg	Leu	Asn	Lys	Asp	Gln	Ser	Lys	His
				100					105					110		
25	Ala	Ile	Asn	Ala	Ala	Phe	Asn	Val	Phe	Ser	Tyr	Arg	Leu	Arg	Asn	Ile
			115					120					125			
	Gly	Val	Gly	Pro	Leu	Gly	Pro	Asp	Ile	Arg	Ser	Ser	Gly	Pro		
30		130					135					140				

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 142 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

45	Met	Asn	Ser	Lys	His	Ser	Tyr	Val	Glu	Leu	Lys	Asp	Lys	Val	Ile	Val
	1			5					10						15	
	Pro	Gly	Trp	Pro	Thr	Leu	Met	Leu	Glu	Ile	Gly	Phe	Val	Gly	Gly	Thr
				20					25					30		
50	Ser	Arg	Asn	Gln	Phe	Leu	Asn	Ile	Pro	Phe	Leu	Ser	Val	Lys	Glu	Pro

	35		40		45
5	Leu Gln Leu Pro Arg Glu Lys Lys Leu Thr Asp Tyr Phe Thr Ile Asp	50	55	60	
	Val Glu Pro Ala Gly His Ser Leu Val Asn Ile Tyr Phe Gln Ile Asp	65	70	75	80
10	Asp Phe Leu Leu Leu Thr Leu Asn Ser Leu Ser Val Tyr Lys Asp Pro	85	90	95	
	Ile Arg Lys Tyr Met Phe Leu Arg Leu Asn Lys Asp Gln Ser Lys His	100	105	110	
15	Ala Ile Asn Ala Ala Phe Asn Val Phe Ser Tyr Arg Leu Arg Asn Ile	115	120	125	
	Gly Val Gly Pro Leu Gly Pro Asp Ile Arg Ser Ser Gly Pro	130	135	140	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

35	Met Gln Pro Ser Met Ser Phe Leu Ile Gly Phe Gly Thr Leu Val Leu	1	5	10	15
	Val Leu Ser Ala Arg Thr Phe Asp Leu Gln Gly Leu Ser Cys Asn Thr	20	25	30	
40	Asp Ser Thr Pro Gly Leu Ile Asp Leu Glu Ile Arg Arg Leu Cys His	35	40	45	
	Thr Pro Thr Glu Asn Val Ile Ser Cys Glu Val Ser Tyr Leu Asn His	50	55	60	
45	Thr Thr Ile Ser Leu Pro Ala Val His Thr Ser Cys Leu Lys Tyr His	65	70	75	80
50	Cys Lys Thr Tyr Trp Gly Phe Phe Gly Ser Tyr Ser Ala Asp Arg Ile	85	90	95	

	Ile	Asn	Arg	Tyr	Thr	Gly	Thr	Val	Lys	Gly	Cys	Leu	Asn	Asn	Ser	Ala	
				100					105							110	
5	Pro	Glu	Asp	Pro	Phe	Glu	Cys	Asn	Trp	Phe	Tyr	Cys	Cys	Ser	Ala	Ile	
			115					120					125				
	Thr	Thr	Glu	Ile	Cys	Arg	Cys	Ser	Ile	Thr	Asn	Val	Thr	Val	Ala	Val	
			130				135					140					
10	Gln	Thr	Phe	Pro	Pro	Phe	Met	Tyr	Cys	Ser	Phe	Ala	Asp	Cys	Ser	Thr	
	145					150					155					160	
	Val	Ser	Gln	Gln	Glu	Leu	Glu	Ser	Gly	Lys	Ala	Met	Leu	Ser	Asp	Gly	
					165					170					175		
15	Ser	Thr	Leu	Thr	Tyr	Thr	Pro	Tyr	Ile	Leu	Gln	Ser	Glu	Val	Val	Asn	
				180					185					190			
	Lys	Thr	Leu	Asn	Gly	Thr	Ile	Leu	Cys	Asn	Ser	Ser	Ser	Lys	Ile	Val	
20			195					200					205				
	Ser	Phe	Asp	Glu	Phe	Arg	Arg	Ser	Tyr	Ser	Leu	Thr	Asn	Gly	Ser	Tyr	
		210					215					220					
25	Gln	Ser	Ser	Ser	Ile	Asn	Val	Thr	Cys	Ala	Asn	Tyr	Thr	Ser	Ser	Cys	
	225					230					235					240	
	Arg	Pro	Arg	Leu	Lys	Arg	Arg	Arg	Arg	Asp	Thr	Gln	Gln	Ile	Glu	Tyr	
					245					250					255		
30	Leu	Val	His	Lys	Leu	Arg	Pro	Thr	Leu	Lys	Asp	Ala	Trp	Glu	Asp	Cys	
				260					265					270			
	Glu	Ile	Leu	Gln	Ser	Leu	Leu	Leu	Gly	Val	Phe	Gly	Thr	Gly	Ile	Ala	
35			275					280					285				
	Ser	Ala	Ser	Gln	Phe	Leu	Arg	Ser	Trp	Leu	Asn	His	Pro	Asp	Ile	Ile	
		290					295					300					
40	Gly	Tyr	Ile	Val	Asn	Gly	Val	Gly	Val	Val	Trp	Gln	Cys	His	Arg	Val	
	305					310					315					320	
	Asn	Val	Thr	Phe	Met	Thr	Trp	Asn	Glu	Ser	Thr	Tyr	Tyr	Pro	Pro	Val	
					325					330					335		
45	Asp	Tyr	Asn	Gly	Arg	Lys	Tyr	Phe	Leu	Asn	Asp	Glu	Gly	Arg	Leu	Gln	
				340					345					350			
	Thr	Asn	Thr	Pro	Glu	Ala	Arg	Pro	Gly	Leu	Lys	Arg	Val	Met	Trp	Phe	
50			355					360					365				

Gly Arg Tyr Phe Leu Gly Thr Val Gly Ser Gly Val Lys Pro Arg Arg  
 370 375 380  
 5 Ile Arg Tyr Asn Lys Thr Ser His Asp Tyr His Leu Glu Glu Phe Glu  
 385 390 395 400  
 Ala Ser Leu Asn Met Thr Pro Gln Thr Ser Ile Thr Ser Gly His Glu  
 405 410 415  
 10 Thr Asp Pro Ile Asn His Ala Tyr Gly Thr Gln Ala Asp Leu Leu Pro  
 420 425 430  
 Tyr Thr Arg Ser Ser Asn Ile Thr Ser Thr Asp Thr Gly Ser Gly Trp  
 435 440 445  
 15 Val His Ile Gly Leu Pro Ser Phe Ala Phe Leu Asn Pro Leu Gly Trp  
 450 455 460  
 Leu Arg Asp Leu Leu Ala Trp Ala Ala Trp Leu Gly Gly Val Leu Tyr  
 465 470 475 480  
 Leu Ile Ser Leu Cys Val Ser Leu Pro Ala Ser Phe Ala Arg Arg Arg  
 485 490 495  
 25 Arg Leu Gly Arg Leu Gln Glu  
 500

(2) INFORMATION FOR SEQ ID NO:27:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 503 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

40 Met Gln Pro Ser Met Ser Phe Leu Ile Gly Phe Gly Thr Leu Val Leu  
 1 5 10 15  
 Val Leu Ser Ala Arg Thr Phe Asp Leu Gln Gly Leu Ser Cys Asn Thr  
 45 20 25 30  
 Asp Ser Thr Pro Gly Leu Ile Asp Leu Glu Ile Arg Arg Leu Cys His  
 35 40 45  
 50 Thr Pro Thr Glu Asn Val Ile Ser Cys Glu Val Ser Tyr Leu Asn His  
 50 55 60

	Thr	Thr	Ile	Ser	Leu	Pro	Ala	Val	His	Thr	Ser	Cys	Leu	Lys	Tyr	His	65	70	75	80
5	Cys	Lys	Thr	Tyr	Trp	Gly	Phe	Phe	Gly	Ser	Tyr	Ser	Ala	Asp	Arg	Ile	85	90	95	
	Ile	Asn	Arg	Tyr	Thr	Gly	Thr	Val	Lys	Gly	Cys	Leu	Asn	Asn	Ser	Ala	100	105	110	
10	Pro	Glu	Asp	Pro	Phe	Glu	Cys	Asn	Trp	Phe	Tyr	Cys	Cys	Ser	Ala	Ile	115	120	125	
	Thr	Thr	Glu	Ile	Cys	Arg	Cys	Ser	Ile	Thr	Asn	Val	Thr	Val	Ala	Val	130	135	140	
15	Gln	Thr	Phe	Pro	Pro	Phe	Met	Tyr	Cys	Ser	Phe	Ala	Asp	Cys	Ser	Thr	145	150	155	160
	Val	Ser	Gln	Gln	Glu	Leu	Glu	Ser	Gly	Lys	Ala	Met	Leu	Ser	Asp	Gly	165	170	175	
20	Ser	Thr	Leu	Thr	Tyr	Thr	Pro	Tyr	Ile	Leu	Gln	Ser	Glu	Val	Val	Asn	180	185	190	
25	Lys	Thr	Leu	Asn	Gly	Thr	Ile	Leu	Cys	Asn	Ser	Ser	Ser	Lys	Ile	Val	195	200	205	
	Ser	Phe	Asp	Glu	Phe	Arg	Arg	Ser	Tyr	Ser	Leu	Thr	Asn	Gly	Ser	Tyr	210	215	220	
30	Gln	Ser	Ser	Ser	Ile	Asn	Val	Thr	Cys	Ala	Asn	Tyr	Thr	Ser	Ser	Cys	225	230	235	240
	Arg	Pro	Arg	Leu	Lys	Arg	Arg	Arg	Arg	Asp	Thr	Gln	Gln	Ile	Glu	Tyr	245	250	255	
35	Leu	Val	His	Lys	Leu	Arg	Pro	Thr	Leu	Lys	Asp	Ala	Trp	Glu	Asp	Cys	260	265	270	
40	Glu	Ile	Leu	Gln	Ser	Leu	Leu	Leu	Gly	Val	Phe	Gly	Thr	Gly	Ile	Ala	275	280	285	
	Ser	Ala	Ser	Gln	Phe	Leu	Arg	Ser	Trp	Leu	Asn	His	Pro	Asp	Ile	Ile	290	295	300	
45	Gly	Tyr	Ile	Val	Asn	Gly	Val	Gly	Val	Val	Trp	Gln	Cys	His	Arg	Val	305	310	315	320
	Asn	Val	Thr	Phe	Met	Thr	Trp	Asn	Glu	Ser	Thr	Tyr	Tyr	Pro	Pro	Val	325	330	335	
50																				

Asp Tyr Asn Gly Arg Lys Tyr Phe Leu Asn Asp Glu Gly Arg Leu Gln  
340 345 350

5 Thr Asn Thr Pro Glu Ala Arg Pro Gly Leu Lys Arg Val Met Trp Phe  
355 360 365

Gly Arg Tyr Phe Leu Gly Thr Val Gly Ser Gly Val Lys Pro Arg Arg  
370 375 380

10 Ile Arg Tyr Asn Lys Thr Ser His Asp Tyr His Leu Glu Glu Phe Glu  
385 390 395 400

Ala Ser Leu Asn Met Thr Pro Gln Thr Ser Ile Ala Ser Gly His Glu  
405 410 415

15 Thr Asp Pro Ile Asn His Ala Tyr Gly Thr Gln Ala Asp Leu Leu Pro  
420 425 430

Tyr Thr Arg Ser Ser Asn Ile Thr Ser Thr Asp Thr Gly Ser Gly Trp  
435 440 445

20 Val His Ile Gly Leu Pro Ser Phe Ala Phe Leu Asn Pro Leu Gly Trp  
450 455 460

25 Leu Arg Asp Leu Leu Ala Trp Ala Ala Trp Leu Gly Gly Val Leu Tyr  
465 470 475 480

Leu Ile Ser Leu Cys Val Ser Leu Pro Ala Ser Phe Ala Arg Arg Arg  
485 490 495

30 Arg Leu Gly Arg Trp Gln Glu  
500

(2) INFORMATION FOR SEQ ID NO:28:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 189 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

His Thr Val Thr Pro Ser Leu Val Phe Leu Cys Leu Leu Ile Pro Gly  
1 5 10 15

50 Leu His Ala Ala Phe Val His Gly Gly Val Pro Arg Glu Ser Tyr Leu  
20 25 30

	Ser	Thr	Pro	Val	Thr	Arg	Gly	Glu	Gln	Thr	Val	Val	Lys	Thr	Ala	Lys
			35					40					45			
5	Phe	Tyr	Gly	Glu	Lys	Thr	Thr	Gln	Arg	Asp	Leu	Thr	Glu	Leu	Glu	Ile
		50					55					60				
	Ser	Ser	Ile	Phe	Ser	His	Cys	Cys	Ser	Leu	Leu	Ile	Gly	Val	Val	Ile
	65					70					75					80
10	Gly	Ser	Ser	Ser	Lys	Ile	Lys	Ala	Gly	Ala	Glu	Gln	Ile	Lys	Lys	Arg
					85					90					95	
	Phe	Lys	Thr	Met	Met	Ala	Ala	Leu	Asn	Arg	Pro	Ser	His	Gly	Glu	Thr
15				100					105					110		
	Ala	Thr	Leu	Leu	Gln	Met	Phe	Asn	Pro	His	Glu	Ala	Ile	Asp	Trp	Ile
			115					120					125			
20	Asn	Gly	Gln	Pro	Trp	Val	Gly	Ser	Phe	Val	Leu	Pro	Leu	Leu	Thr	Thr
	130						135					140				
	Asp	Phe	Glu	Ser	Pro	Gly	Lys	Glu	Phe	Met	Asp	Gln	Ile	Lys	Leu	Val
	145					150				155						160
25	Ala	Ser	Tyr	Ala	Gln	Met	Thr	Thr	Tyr	Thr	Thr	Ile	Lys	Glu	Tyr	Leu
					165					170					175	
	Ala	Glu	Cys	Met	Asp	Ala	Thr	Leu	Thr	Ile	Pro	Val	Val			
30				180					185							

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

45	His	Thr	Val	Thr	Pro	Ser	Leu	Val	Phe	Leu	Cys	Leu	Leu	Ile	Pro	Gly
	1				5					10					15	
	Leu	His	Ala	Ala	Phe	Val	His	Gly	Gly	Val	Pro	Arg	Glu	Ser	Tyr	Leu
			20					25					30			
50	Ser	Thr	Pro	Ile	Thr	Arg	Gly	Glu	Gln	Thr	Val	Val	Lys	Thr	Ala	Glu
			35				40						45			



Phe Tyr Gly Glu Lys Thr Thr Gln Arg Asp Leu Thr Glu Leu Glu Ile  
 50 55 60  
 Ser Ser Ile Phe Ser His Cys Cys Ser Leu Leu Ile Gly Val Val Ile  
 5 65 70 75 80  
 Gly Ser Ser Ser Lys Ile Lys Ala Glu Ala Glu Gln Ile Lys Lys Arg  
 85 90 95  
 Phe Lys Thr Met Met Ala Ala Val Asn Arg Pro Ser His Gly Glu Thr  
 10 100 105 110  
 Ala Thr Leu Leu Gln Met Phe Asn Pro His Glu Ala Ile Asp Trp Ile  
 115 120 125  
 15 Asn Gly Gln Pro Trp Val Gly Ser Phe Val Leu Ser Leu Leu Thr Thr  
 130 135 140  
 Asp Phe Glu Ser Pro Gly Lys Glu Phe Met Asp Gln Ile Lys Leu Val  
 20 145 150 155 160  
 Ala Ser Tyr Ala Gln Met Thr Thr Tyr Thr Thr Ile Lys Glu Tyr Leu  
 165 170 175  
 25 Ala Glu Cys Met Asp Ala Thr Leu Thr Ile Pro Val Val  
 180 185

(2) INFORMATION FOR SEQ ID NO:30:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

40 His Thr Val Thr Pro Ser Leu Val Phe Leu Cys Leu Leu Ile Pro Gly  
 1 5 10 15  
 Leu His Ala Ala Phe Val His Gly Gly Val Pro Arg Glu Ser Tyr Leu  
 45 20 25 30  
 Ser Thr Pro Ile Thr Arg Gly Glu Gln Thr Val Val Lys Thr Ala Lys  
 35 40 45  
 50 Phe Tyr Gly Glu Lys Thr Thr Gln Arg Asp Leu Thr Glu Leu Glu Ile  
 50 55 60

Ser Ser Ile Phe Ser His Cys Cys Ser Leu Leu Ile Gly Val Val Ile  
 65 70 75 80  
 Gly Ser Ser Ser Lys Ile Lys Ala Gly Ala Glu Gln Ile Lys Lys Arg  
 85 90 95  
 Phe Lys Thr Met Met Ala Ala Leu Asn Arg Pro Ser His Gly Glu Thr  
 100 105 110  
 Ala Thr Leu Leu Gln Met Phe Asn Pro His Glu Ala Ile Asp Trp Ile  
 115 120 125  
 Asn Gly Gln Pro Trp Val Gly Ser Phe Val Leu Ser Leu Leu Thr Thr  
 130 135 140  
 Asp Phe Glu Ser Pro Gly Lys Glu Phe Met Asp Gln Ile Lys Leu Val  
 145 150 155 160  
 Ala Ser Tyr Ala Gln Met Thr Thr Tyr Thr Thr Ile Lys Glu Tyr Leu  
 165 170 175  
 Ala Glu Cys Met Asp Ala Thr Leu Thr Ile Pro Val Val  
 180 185

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Thr Met Ser Ser Thr Ala Leu Thr His Leu Leu Asn Arg Leu Ser His  
 1 5 10 15  
 Thr Ile Thr Lys Gly Asp Ser Phe Val Ile Asn Leu Asp Tyr Ser Ser  
 20 25 30  
 Trp Cys Asn Gly Phe Arg Pro Glu Leu Gln Ala Pro Ile Cys Arg Gln  
 35 40 45  
 Leu Asp Gln Met Phe Asn Cys Gly Tyr Phe Phe Arg Thr Gly Cys Thr  
 50 55 60  
 Leu Pro Cys Phe Thr Thr Phe Ile Ile Gln Asp Arg Phe Asn Pro Pro  
 65 70 75 80

Tyr Ser Leu Ser Gly Glu Pro Val Glu Asp Gly Val Thr Cys Ala Val  
 85 90 95  
 5 Gly Thr Lys Thr Met Gly Glu Gly Met Arg Gln Lys Leu Trp Thr Ile  
 100 105 110  
 Leu Thr Ser Cys Trp Glu Ile Ile Ala Leu Arg Glu Ile Asn Val Thr  
 115 120 125  
 10 Phe Asn Ile Leu Gly Gln Gly Asp Asn Gln Thr Ile Ile Ile His Lys  
 130 135 140  
 Ser Ala Ser Gln Asn Asn Gln Leu Leu Ala Glu Arg Ala Leu Gly Ala  
 145 150 155 160  
 15 Leu Tyr Lys His Ala Arg Leu Ala Gly His Asn Leu Lys Val Glu Glu  
 165 170 175  
 Cys Trp Val Ser Asp Cys Leu Tyr Glu Tyr Gly Lys Lys Leu Phe Phe  
 180 185 190  
 20 Arg Gly Val Pro Val Pro Gly Cys Leu Lys Gln Leu Ser Arg Val Thr  
 195 200 205  
 25 Asp Ser Thr Gly Glu Leu Phe Pro Asn Leu Tyr Ser Lys Leu Ala Cys  
 210 215 220  
 Leu Thr Ser Ser Cys  
 225

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Thr Gly Pro Ser Ser Leu Val Asp Ser Leu Glu Asp Glu Glu  
 1 5 10 15  
 Asp Pro

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Ile Tyr Pro Gln Leu Pro Ser Ala Pro Thr Ala Asp Glu Trp Asp  
1 5 10 15

Ile Ile Pro

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Asn Ser Lys His Ser Tyr Val Glu Leu Lys Gly Lys Val Ile Val  
1 5 10 15

Pro Gly

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Leu Arg Asn Ile Gly Val Gly Pro Leu Gly Pro Asp Ile Arg Ser  
1 5 10 15

10 Ser Gly Pro

(2) INFORMATION FOR SEQ ID NO:36:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Leu Ser Cys Asn Thr Asp Ser Thr Pro Gly Leu Ile Asp Leu Glu  
1 5 10 15

30 Ile Arg

(2) INFORMATION FOR SEQ ID NO:37:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg Ser Lys Leu Arg Arg Arg Arg Asp Thr Gln Gln Ile Glu Tyr  
1 5 10 15

Leu Val

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Leu Ile Ser Leu Cys Val Ser Leu Pro Ala Ser Phe Ala Arg Arg Arg  
1                    5                    10                    15

Arg Leu Gly Arg Trp Gln Glu  
                    20

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Pro Pro Lys Arg Arg Leu Val Asp Asp Ala Asp Ala Met Glu Asp  
1                    5                    10                    15

Gln Asp

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

10 Met Glu Asp Gln Asp Asp Leu Tyr Glu Pro Pro Ala Ser Leu Pro Lys  
1 5 10 15  
Leu Pro

15 (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

30 Glu Leu Ser Gly Glu Ile Ser Ala Ile Met Arg Met Ile Gly Val Thr  
1 5 10 15  
Gly Leu Val

35

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGGAGGCTC AATGGCAACG

20

5 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTTATGGTAT GATGTCCAC

20

25 (2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATCGAATCAC CATGAATTCA AAGC

24

45 (2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

10

GTCAGTATTG CAACTAAGGC

20

(2) INFORMATION FOR SEQ ID NO:46:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

30

GCACGCAATT AATGCAGC

18

(2) INFORMATION FOR SEQ ID NO:47:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

45

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

50

CAGTGTAGGC CTAAGCTTGT G

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGTTGAGAA GGCGGCGTAG

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGTACGGTT TATTCCTGC

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGACCATGAG CTCAACGGC

19

(2) INFORMATION FOR SEQ ID NO:51:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GCATGATGAT GTTAAGCAGG C

21

(2) INFORMATION FOR SEQ ID NO:52:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TTCATACAGT AACGCCCAGC

20

(2) INFORMATION FOR SEQ ID NO:53:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

15

GCAACTACAG GGATTGTAAG GG

22

(2) INFORMATION FOR SEQ ID NO:54:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

35

GCCTTGTGTT TCTATGTTTG C

21

(2) INFORMATION FOR SEQ ID NO:55:

40

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

50

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCATCCATAC ATTCTGCGAG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGAATTCGCA CGCAATTAAT GCAGC

25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCTACTCGAG CGGTACGGTT TATTCCTGC

29

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCCCCGGGC AATGTACTGC AGTTTCGGG ACT

33

15 (2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGCCCCGGGT TATTCCTGCC ACCGGCCGA

29

35 (2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGCCACCCG GGAGACGCCT GATTGAT

27

(2) INFORMATION FOR SEQ ID NO:61:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

15

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

20

CGGATCCCGG GCTAGTTTAG ACCAGTCACT CC

32

(2) INFORMATION FOR SEQ ID NO:62:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

40

GGCCATATGC GCCCGGGCCC ATCGAGTCTG GTCGACTCCC TG

42

(2) INFORMATION FOR SEQ ID NO:63:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTCGAGCCCG GGTATGGTA TGATGTCCCA CTCATC

36

10

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CGAATCCCCG GGAATTCAAA GCATTCCTA

29

30

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCCCCCGGG CAGTATTGCA ACTAACGG

28

50